

1	6599	99.9	6643	1	V31881	Human Down syndrome
2	6508.8	94.0	6613	1	V31888	Human Down syndrome
3	1411.2	17.3	2173	1	V31887	Mouse Down syndrome
4	670.2	10.1	842	1	V31885	Mouse Down syndrome
5	541	8.2	1453	1	V27207	cDNA clone ethb00100
6	502	7.6	888	1	V31986	Mouse Down syndrome
7	388	5.9	388	1	V31982	Human Down syndrome
8	66.4	1.0	6000	1	O86478	Human ptp-OB. Protein
9	66.4	1.0	6000	1	T85389	Human protein tyrosine
10	62	0.9	12001	1	O76213	HSV L/ST region. H
11	62	0.9	4257	1	V10362	Infected cell protein
12	62	0.9	117213	1	V62176	HSV-2 strain SB5 C
13	62	0.9	4257	1	V68520	The nucleotide sequence
14	61.6	0.9	4403	1	O47927	Paired basic amino acid
15	61.6	0.9	2218	1	O47929	Paired basic amino acid
16	60.4	0.9	8438	1	O73500	DNA encoding pseudovirus
17	60.4	0.9	4020	1	T91361	Orf virus genomic
18	60.4	0.9	117213	1	V62176	HSV-2 strain SB5 C
19	60.2	0.9	1026	1	O66091	MUSDUJNK, a sample
20	59.4	0.9	12001	1	O76213	HSV L/ST region. H
21	59.4	0.9	4257	1	V10362	Infected cell protein
22	59.4	0.9	4257	1	V68520	The nucleotide sequence
23	58.8	0.9	44377	1	T78508	Platenolide synthase
24	58.8	0.9	44377	1	T80414	Platenolide synthase
25	58.4	0.9	4504	1	O36467	M. scrofulaceum sh
26	58.4	0.9	3946	1	T93610	Mycobacterium tuberculosis
27	58.2	0.9	2974	1	O79530	Partial FRAKE region
28	57.8	0.9	6604	1	V31881	Human Down syndrome
29	57.8	0.9	6413	1	V31888	Human Down syndrome
30	57.4	0.9	6803	1	T85473	Genomic hNET sequence
31	57.4	0.9	1743	1	T85537	hNET cDNA sequence
32	57.4	0.9	1743	1	V16506	cDNA encoding human
33	57.4	0.9	1974	1	V16345	Nucleotide sequence
34	57.4	0.9	6803	1	V16305	Genomic DNA encoding
35	57.2	0.9	1581	1	V33378	Nucleotide sequence
36	57.2	0.9	1583	1	V33377	Nucleotide sequence
37	56.6	0.9	2823	1	T35233	Natural killer lymphocyte
38	56.2	0.9	5357	1	T18551	Human polycystic kidney
39	56.2	0.9	5357	1	T94108	Human PKD1 locus B
40	56.2	0.9	5356	1	T94101	Human PKD1 gene. H
41	56	0.8	1611	1	V62479	Human MAP kinase.
42	55.8	0.8	2992	1	T67285	Soluble starch synthase
43	55.6	0.8	43280	1	T80413	Tylectone synthase

Qy 1 tgactgaagccgagacacgcygcaagaatgaagcctgacccgcgcgcctgtctgtcatgtcgg 60

Ddb 1 TGACTGAGGCCGAGACACGCGCAAGATGAGCCTCCCCGCGCGCTGCTGCTGATGCGG 60

C	1	66.4	1.0	6000	2	US-08-348-006B-6	Sequence 6, Appl
C	2	66.4	1.0	6000	4	US-08-800-825A-5	Sequence 6, Appl
C	3	66.4	1.0	6000	5	PCT-US94-1016A-6	Sequence 6, Appl
C	4	62.2	0.9	801	4	US-08-770-379-16	Sequence 16, Appl
C	5	62	0.9	12001	3	US-08-458-568A-11	Sequence 11, Appl
C	6	62	0.9	4257	4	US-08-650-473-1	Sequence 1, Appl
C	7	61.5	0.9	4403	5	US-08-284-941-1	Sequence 1, Appl
C	8	61.6	0.9	4403	5	PCT-US93-02147A-1	Sequence 1, Appl
C	9	60.4	0.9	8438	1	US-07-945-283-1	Sequence 1, Appl
C	10	60.2	0.9	1026	1	US-07-975-526-6	Sequence 6, Appl
C	11	59.4	0.9	12001	3	US-08-438-568A-11	Sequence 6, Appl
C	12	59.4	0.9	4257	4	US-08-650-473-1	Sequence 11, Appl
C	13	58.8	0.9	44377	4	US-08-804-227C-7	Sequence 1, Appl
C	14	56.6	0.9	2823	2	US-08-358-0C8A-1	Sequence 7, Appl
C	15	55.6	0.8	43280	4	US-08-804-227C-1	Sequence 1, Appl
C	16	55.4	0.8	1610	1	US-08-056-051-5	Sequence 5, Appl
C	17	55.4	0.8	803	1	US-07-928-611-12	Sequence 12, Appl
C	18	55.4	0.8	1610	1	US-07-928-611-12	Sequence 12, Appl
C	19	55.4	0.8	803	4	US-08-487-811A-12	Sequence 12, Appl
C	20	55.4	0.8	1610	4	US-08-487-811A-21	Sequence 21, Appl
C	21	55.4	0.8	803	5	PCT-US93-07370-12	Sequence 12, Appl
C	22	55.4	0.8	1610	5	PCT-US93-07370-21	Sequence 21, Appl
C	23	55.2	0.8	5117	5	PCT-US93-05512-1	Sequence 1, Appl
C	24	55	0.8	936	2	US-08-018-977C-4	Sequence 4, Appl
C	25	54.2	0.8	5467	1	US-07-745-056A-12	Sequence 12, Appl
C	26	54.2	0.8	7362	3	US-08-455-543A-7	Sequence 7, Appl
C	27	54.2	0.8	7175	3	US-08-455-543A-8	Sequence 8, Appl
C	28	54.2	0.8	1550	4	US-08-609-443B-17	Sequence 17, Appl
C	29	54.2	0.8	7362	4	US-08-193-078B-7	Sequence 7, Appl
C	30	54.2	0.8	7175	4	US-08-193-078B-8	Sequence 8, Appl
C	31	54.2	0.8	7362	4	US-08-223-305C-7	Sequence 7, Appl
C	32	54.2	0.8	7175	4	US-08-223-305C-8	Sequence 8, Appl
C	33	54.2	0.8	7362	4	US-08-149-097D-7	Sequence 7, Appl
C	34	54.2	0.8	7175	4	US-08-149-097D-8	Sequence 8, Appl
C	35	54.2	0.8	5457	3	US-08-311-353-12	Sequence 12, Appl
C	36	53.8	0.8	5457	3	US-08-306-691B-14	Sequence 14, Appl
C	37	53.4	0.8	2483	2	US-08-464-340A-3	Sequence 3, Appl

[illegible]

	Query Match	1.0%	Score 66.4	DB 2	Length 6000	
	Best Local Similarity	47.7%	Pred. No. 7.5e-07			
	Matches 227; Conservative	0;	Mismatches 246;	Indels 3;	Gaps 1	
QY	3597	tacaccctggaacaactgaatgaagttcactcaagtcagcgccygtgylgcagacctgtaac	3656			
Db	1721	TGAGTGATGGAGACTTAAGGCCCAACAGSAGTACGCCTTCGCGCTGGGGCCGCTCG	1780			
QY	3657	cgggccgycagcaggggccttcltcltcaagaatacaaccaactcgcgaqaatlgyccc	3716			
Db	1781	CCGCAAGGCGCTGTGGCGCCTTCACCCCGCGTGTGGGGCAAGCGCACGTGCAGTCCAACC	1840			
QY	3717	agttaccccccccaagtatgltccaaagcatagcaaatcacccagaagaatcataatatccc	3776			

Db 1841 TCAGCCCCCTCAAGAGCTTAATGTCTCAGCGTCCGCTCAGCGCATTTTGTAGT 1900
Qy 3777 TgTcacaacttccaaagaccttgaaatggaattctcaggggttcaagatcattac 3836
Db 1901 TGGCGCCCGCCGCGCCGCGAAACGACACGGGGCCCTGGGTGCTACAGGCTCGGTAC 1960
Qy 3837 tg---ggcaaacctcatgagagagagcttggtgagatataaacaatcacaccacag 3893
Db 1961 CGACCGCTGGGCTCAGAGAGACCCGAGACCCCAAGAGGTGAACGGCATCCCCACACAC 2020
Qy 3894 ccttaactggaactgagagagcttgaaagatcaccaactacagatcagatgtgccc 3953
Db 2021 ACTCAGATCTCTCTGGAGCCCTTGAGAGGTGAGACCCAGTACCGCATCAGCATGTGCT 2080
Qy 3954 ttaccacgcagcagagagaggttcagagatcagacatctcaccgcagcaagagat 4013
Db 2081 CACACAGAGGTGGAGCCAGGCGCCGAGAGCTCGCCGCTGCTCCGACCCGAGAGAT 2140
Qy 4014 gtccagagctcccgaggtgtgagagcagcgagcctcagctcagtgctt 4069
Db 2141 GTGCCAGGCTGCGCCGCGGAGAGGTGAGGCGGAGCGCTCAACGCTACGGCCAT 2196

RESULT 2

US-08-800-825A-6
Sequence 6, Application US/0880825A
Patent No. 586397

GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800.825A
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-800-825A-6

Query Match 1.0% Score 56.4; DB 4; Length 6000;

Best Local Similarity 47.7% Pred No. 7.5e-07;
Matches 227; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

Qy 3597 tacacccctgacaacactgataatgactcagatagaccctcagtgatgacagcctgtaac 3656

Db 1721 TAGTGTGTGAGAGACTGATGACCCCAACAGGAGTACGGCTTCCGCTGCGCGCCGCTCG 1780
Qy 3657 cgggcccagcaggggagctctctctcaggaatcaltcacaccacatctcagagatgtccc 3716
Db 1781 CCGCAGGGGCTGGGCGCTTTCACCCCGGTGTGCGGCAAGCCAGCTCAGTCCAAACCG 1840
Qy 3717 agttaccccccgaaaatgtctcaagccatagacaatcaccccgaaagatataatcc 3776
Db 1841 TCAGCCCCCTCAAGACTTAATGTCTCAGCGTCCGCTCAGCGCATTTTGTAGT 1900
Qy 3777 TgTcacaacttccaaagaccttgaaatggaattctcaggggttcaagatcattac 3836
Db 1901 TGGCGCCCGCCGCGCCGCGAAACGACACGGGGCCCTGGGTGCTACAGGCTCGGTAC 1960
Qy 3837 tg---ggcaaacctcatgagagagagcttggtgagatataaacaatcacaccacag 3893
Db 1961 CGACCGCTGGGCTCAGAGAGACCCGAGACCCCAAGAGGTGAACGGCATCCCCACACAC 2020
Qy 3894 ccttaactggaactgagagagcttgaaagatcaccaactacagatcagatgtgccc 3953
Db 2021 ACTCAGATCTCTCTGGAGCCCTTGAGAGGTGAGACCCAGTACCGCATCAGCATGTGCT 2080
Qy 3954 ttaccacgcagcagagagaggttcagagatcagacatctcaccgcagcaagagat 4013
Db 2081 CACACAGAGGTGGAGCCAGGCGCCGAGAGCTCGCCGCTGCTCCGACCCGAGAGAT 2140
Qy 4014 gtccagagctcccgaggtgtgagagcagcgagcctcagctcagtgctt 4069
Db 2141 GTGCCAGGCTGCGCCGCGGAGAGGTGAGGCGGAGCGCTCAACGCTACGGCCAT 2196

RESULT 3

PCT-US94-10166-6
Sequence 6, Application PCT/US9410166

GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN III
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10166
FILING DATE: 09-SEPT-1994
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35403
REFERENCE/DOCKET NUMBER: 18992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
TELEX: 138825

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
TYPE: nucleic acid

C	45	67.8	1.0	4233	12	HSU75308
C	44	67.8	1.0	10144	10	HUHHMGIT
C	43	67.8	1.0	1829	5	S46000
C	42	68.2	1.0	42301	43	AC005943
C	41	68.2	1.0	42301	43	AC005943
C	40	68.8	1.0	1560	17	HS21E
C	39	69.6	1.1	154746	17	HS21HG52
C	38	69.6	1.1	3957	6	A45258
C	37	70.4	1.1	73	11	HS298234
C	36	70.4	1.1	73	11	HS298234
C	35	71.6	1.1	2764	17	HSBBICPB
C	34	71.8	1.1	2026	5	GG47276
C	33	72	1.1	38939	42	AC004678
C	32	72	1.1	8113	17	HSBBICPBA
C	31	72	1.1	38939	11	AC004678
C	30	73.2	1.1	20000	18	AC004670
C	29	73.4	1.1	2685	42	HUMHBA3
C	28	73.4	1.1	43053	42	HSBG1
C	27	73.4	1.1	2685	11	HUMHBA3
C	26	74.8	1.1	43574	11	HSBG1
C	25	74.8	1.1	8113	17	HSBBICPBA
C	24	74.8	1.1	135301	17	BHYICGN
C	23	75.8	1.1	3252	42	HSTAR113
C	22	75.8	1.1	3252	18	CEY39B6
C	21	78	1.2	33159	18	CEY39B6
C	19	296	4.5	154561	42	AF064862
C	18	296	4.5	154561	42	AF064862
C	17	296	4.5	154561	11	AF064862
C	16	296	4.5	154561	11	AF064862
C	15	307.2	4.7	121019	42	AF042091
C	14	307.2	4.7	155407	42	AF042091
C	13	307.2	4.7	121019	11	AF042090
C	12	307.2	4.7	155407	42	AF042090
C	11	319.4	4.8	120007	11	AF064864
C	10	319.4	4.8	120007	11	AF064864
C	9	358.8	5.4	430	38	G36691
C	8	495.4	7.5	109686	42	AF043945
C	7	495.4	7.5	109686	11	AF043945
C	6	699	10.6	721	42	HUMT291E03
C	5	699	10.6	721	11	HUMT291E03
C	4	6110	92.5	6110	42	AF023449
C	3	6110	92.5	6110	11	AF023449
C	2	6212	94.1	6413	42	AF023450
C	1	6212	94.1	6413	11	AF023450
C	45	67.8	1.0	4233	12	HSU75308
C	44	67.8	1.0	10144	10	HUHHMGIT
C	43	67.8	1.0	1829	5	S46000
C	42	68.2	1.0	42301	43	AC005943
C	41	68.2	1.0	42301	43	AC005943
C	40	68.8	1.0	1560	17	HS21E
C	39	69.6	1.1	154746	17	HS21HG52
C	38	69.6	1.1	3957	6	A45258
C	37	70.4	1.1	73	11	HS298234
C	36	70.4	1.1	73	11	HS298234
C	35	71.6	1.1	2764	17	HSBBICPB
C	34	71.8	1.1	2026	5	GG47276
C	33	72	1.1	38939	42	AC004678
C	32	72	1.1	8113	17	HSBBICPBA
C	31	72	1.1	38939	11	AC004678
C	30	73.2	1.1	20000	18	AC004670
C	29	73.4	1.1	2685	42	HUMHBA3
C	28	73.4	1.1	43053	42	HSBG1
C	27	73.4	1.1	2685	11	HUMHBA3
C	26	74.8	1.1	43574	11	HSBG1
C	25	74.8	1.1	8113	17	HSBBICPBA
C	24	74.8	1.1	135301	17	BHYICGN
C	23	75.8	1.1	3252	42	HSTAR113

RESULT	1			
AF023450				
LOCUS	AF023450	6413 bp	mrna	PRI 02-JUN-1998
DEFINITION	Human sapiens CH2-52	Down syndrome cell	adhesion molecule (DSCAM)	
DEFINITION	mrna, complete cds.			
ACCESSION	AF023450			
MD	93169/67			

ORGANISM	JOURNAL REFERENCE AUTHORS	TITLE
<i>Homo sapiens</i>	Unpublished	
Eukaryotae: Metazoa: Chordata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo	1 (bases 1 to 6413)	
<i>Yamkkaava, K., Huo, Y.-K., Haendel, M. A., Hubert, R., Chen, X.-N., Lyons, G. E., and Korenberg, J. R.</i>	DSGAM: A Novel Member of the Immunoglobulin Superfamily Maps in Down Syndrome Region and is Involved in the Development of the Nervous System	
<i>Yamkkaava, K., Huo, Y.-K., Haendel, M. A., Hubert, R., Chen, X.-N., Lyons, G. E., and Korenberg, J. R.</i>	2 (bases 1 to 6413)	
Direct Submission		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 1999, 09:42:16 : Search time 795.19 Seconds
(without alignments)
12658.348 Million cell updates/sec

Title: US-08-956-991-1

Perfect score: 6604

Sequence: 1 tgcattggcgcgcgcgcacgcg.....gaaatgcacaaatatatt 6604

Scoring table: IDENTITY_NUC

Searched: 2002476 seqs, 762712212 residues

Database: ESR:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: qb_est1:*
11: qb_est2:*
12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
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16: qb_est7:*
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19: qb_est10:*
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23: em_est10:*
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34: qb_est15:*
35: qb_est16:*
36: qb_est17:*
37: qb_est18:*
38: qb_est19:*
39: qb_est20:*
40: qb_est21:*
41: qb_est22:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	415.8	6.3	439	41	A1243628	qN88a03.x
C 2	397.4	6.0	419	39	A1094516	A1094516 ov63f11.s

C 3	374.2	5.7	510	13	N80326	N80326 y291f03.r1
C 4	358.8	5.4	430	12	N64532	N64532 y291f03.s1
C 5	343.8	5.2	355	34	HS1003472	A1003472 H.sapiens
C 6	318	4.8	321	13	HSC2WH042	Z41519 H.sapiens
C 7	303.4	4.6	307	39	A1051251	A1051251 oy49e04.x
C 8	288	4.4	310	12	HSC2XA021	F13426 H.sapiens
C 9	278	4.2	294	13	HSC2WH041	Z45894 H.sapiens
C 10	254.8	3.9	337	15	AA170935	AA170935 ms45h05.r
C 11	242.4	3.7	252	12	HSC2XA022	F09100 H.sapiens
C 12	187	2.8	187	36	AA878733	AA878733 oe80d01.s
C 13	187	1.9	646	41	A1106884	A1106884 GR06134.5
C 14	113.4	1.7	298	17	AA325603	AA325603 EST8915
C 15	90.6	1.4	786	41	AA697364	AA697364 H102328.5
C 16	77.6	1.2	1056	13	W42205	W42205 mc69e09.r1
C 17	73.8	1.1	759	13	W28277	W28277 44q8 Human
C 18	73.2	1.1	1257	13	W98479	W98479 mg20c12.r1
C 19	73	1.1	1049	13	W42199	W42199 mc69c09.r1
C 20	72	1.1	1070	14	W29531	W29531 mc03g12.r1
C 21	71.8	1.1	1161	13	W41959	W41959 mc68b10.r1
C 22	70.8	1.1	1145	14	W29156	W29156 mb96a09.r1
C 23	70.4	1.1	1162	13	W42215	W42215 mc69h10.r1
C 24	70.2	1.1	1311	14	W15735	W15735 mb53g03.r1
C 25	70.2	1.1	459	41	A1285778	A1285778 qu56b02.x
C 26	69.8	1.1	1145	14	AA028476	AA028476 m121e10.r
C 27	69.6	1.1	453	14	AA008005	AA008005 mg64c12.r
C 28	68.6	1.0	413	41	A1249175	A1249175 qb68904.x
C 29	68.4	1.0	453	14	AA008005	AA008005 mg64c12.r
C 30	67.4	1.0	1137	14	W29429	W29429 mb96g03.r1
C 31	67.4	1.0	363	41	AA697625	AA697625 H102894.5
C 32	66.2	1.0	1461	14	W15723	W15723 mb53c01.r1
C 33	66.2	1.0	1208	14	W29297	W29297 mb99e03.r1
C 34	66	1.0	1084	15	AA028875	AA028875 mh90d12.r
C 35	65.6	1.0	830	13	W28827	W28827 52c5 Human
C 36	65.4	1.0	1243	13	W42204	W42204 mc69g11.r1
C 37	65.4	1.0	424	41	A1270350	A1270350 qu86g12.x
C 38	64.6	1.0	859	13	W28841	W28841 52d7 Human
C 39	64.6	1.0	1044	13	W42217	W42217 mc69h12.r1
C 40	64.4	1.0	1100	15	AA203745	AA203745 zx53f05.r
C 41	64.2	1.0	763	13	W25843	W25843 13h6 Human
C 42	64.2	1.0	407	40	A1250825	A1250825 gx04f05.x
C 43	63.4	1.0	1111	13	W41963	W41963 mc68d10.r1
C 44	63.4	1.0	1286	13	W42216	W42216 mc69h11.r1
C 45	63	1.0	1068	14	W29367	W29367 mc03h09.r1

ALIGNMENTS

RESULT 1
A1243628 439 bp mRNA EST 01-DEC-1998
LOCUS qN88a03.x1 SOURCE NPL-T-GRC.S1 Homo sapiens cDNA clone
DEFINITION IMAGE1654028 3', mRNA sequence.

ACCESSION A1243628
NID q3839025
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 439)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through INMIL; contact the
IMAGE Consortium (info@image.nih.gov) for further information.
Insert Length: 476 Std Error: 0.00
Seq primer: -40UP from Gibco.


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1 MetTrpIleLeuAlaLeuSerLeuPheGlnSerPheAlaAsnValPheSer 17
453 ATGTGGATTACTGGCTCTCTCCCTTGTCCAGACTTCGGCAAGTTTTCAG 502
17 rGluAspLeuHisSerSerLeuTyrPheValAsnAlaSerLeuGlnIuV 34
503 TGAAGACCTACACTCCAGCTTACTTCTCTCATCATCATCTCTCGCAAGAG 552
34 aValAlaPheAlaSerThrThrGlyThrLeuValProCysProAlaAlaGly 50
553 TAGTGTTCCTCCAGCACACGGGAGCTGTGCTCCCTGCCCGCCAGCAGC 602
51 IleProProValThrLeuArgTrpTyrLeuAlaThrGlyIleIleTyr 67
603 ATCCCTCCCTGACTCTCAGATGTGACTAGCCACGGGAGGAGAGACTCTA 652
67 rAspValProGlyIleArgHisValHisProAsnGlyThrLeuGlnIleP 84
653 CGATGTCCCGGGATCCGCACGTCACCCCAACGGCAGCTCTCCAATTT 702
84 heProPheProSerSerPheSerThrLeuIleHisAsnThrTyr 100
703 TCCCTTCCCTCCTTCAGACTTACACTTAATCCATGA AATACTTAT 752
101 TyrCysThrAlaGluAsnProSerGlyLysIleArgSerGlnAspValH 117
753 TATTGCACAGCTCAAAATCCTTCAGGAAATAGAAATCAGATGTCACA 802
117 sIleLysAlaValLeuArgIuProTyrThrValArgValGluAspGln 134
803 CATCAACGCTGTTTACGGGAGCCCTAATACAGTCGCTGTGGAGACCAGA 852
134 ysthMetArgGlyAsnValAlaValPheLysCysIleIleProSerSer 150
853 AAACCATAGAGAGCAATGTTCGGCTTCAAGTGCATTAATCCCTCTCTG 902
151 ValGluAlaTyrIleThrValValSerTrpGluLysAspThrValSerI 167
903 GTGGAGGCTATACATCACTGCTCTCAATGGAGAAAGACACTGTTTCACT 952
167 uValSerGlySerArgPheLeuIleThrSerThrGlyAlaLeuTyrIle 184
953 TGTCTCAGGATCTAGATTTCATCATCATCACCGGAGCCTTGATATTA 1002
184 yAspValGlnAsnGluAspGlyLeuTyrAsnTyrArgCysIleThrArg 200
1003 AAGATGTACACAATGAAGATGATTGTATTAACCGCTGCATCAGCCGG 1052
201 HisArgTyrThrGlyIuThrArgGlnSerAsnSerAlaArgLeuPheVa 217
1053 CATCATACACCGGAGAGACGAGCAGCAGCAACAGCGCCAGACTTTTGT 1102
217 lSerAspProAlaAsnSerAlaProSerIleLeuAspGlyPheAspHisA 234
1103 ATCAACACCCAGGAACCTCAGCCCATTCATCTGATGGTTGACCATC 1152
234 rGlyAlaMetAlaGlyIuArgValGluLeuProCysLysAlaLeuGly 250
1153 GCAAAGCCATGGCTGGCAGCGTGTGGAGCTGCTTCMAAGCGCTCGGG 1202
251 HisProGluProAspTyrArgTrpLeuLysAspAsnMetProLeuGluLe 267
1203 CACCTGACCCAGATTACCGCTGGCTGAAGGCAACATGCCCTGGAAC 1252
267 uSerGlyArgPheGlnLysThrValThrGlyLeuLeuIleGluAsnIleA 284
1253 TTCAGGAGGAGTTCAGAAAGACCGTCGACGGGCTCTCATATGAGAACATTC 1302
284 rProProSerAspSerGlySerTyrValCysGluValSerAsnArgTyrGly 300
1303 GCCCTTCGAGCTACGACAGCTATGTTTGAGATGTCACACAGATACGGA 1352
301 ThrAlaLysValIleGlyArgLeuTyrValLysGlnProLeuLysAlaTh 317

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1353 ACTGTAAGGTGATAGCCCGCTGTACGTGAAGAACGCCACTGAAGCCAC 1402
317 rIleSerProArgLysValLysSerSerValGlySerGlnValSerLeuS 334
1403 CATCAGTCCCGAGGAGAGCTTAAAGCAGCGTGGTAACCAAGTTCTTGT 1452
334 eCysSerValThrGlyThrGluAspGlnIuLeuSerTrpTyrArgAsn 350
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351 GlyGluIleLeuAsnProGlyLysAsnValArgIleThrGlyIleAsnH 367
1503 GGTGAATTCCTCAACCTGGAAAAAATGTAGGATACAGGGGTACACCA 1552
367 sGluAsnLeuIleMetAspHisMetValLysSerAspGlyAlaIleArg 384
1553 CGAAACCTTATATGATGATACATGCTCAAAAGTGAACGGGGCGCATACC 1602
384 lncysPheValArgLysAspLysLeuSerAlaGlnAspTyrValGlnVal 400
1603 AGTCTTTGTGCGCAAGACAGCAAGCTGTCCGCTCAAGACTATGTCAAGTGT 1652
401 ValLeuGluAspGlyThrProLysIleIleSerAlaPheSerGluLysVa 417
1653 GTCTTGAAGATGAPCTCCCAAAATTAATTTCTGCTTGTGTAAGAGT 1702
417 lValSerProAlaGluProValSerLeuMetCysAsnValLysGlyThrP 434
1703 GGTAGTGTCCACAGACCGCGTTCCTTATGTGCACAGTGAAGAGGAACAC 1752
434 rOleuProThrIleThrTrpThrLeuAspAspProIleLeuLysGly 450
1753 CTTTGCCACAGATCAGCGTGAACCTGGACGATGACCCGATTTCTCAAGGT 1802
451 GlySerHisArgIleSerGlnMetIleThrSerGluGlnAsnValIleSe 467
1803 GGCATATCACCGCATCAGCCAGCATGATCAGTCGAGGAGGAACGTGTACAG 1852
467 rTyrLeuAsnIleSerSerGlnValArgAspGlyGlyAlaTyrArg 484
1853 CTACCTGAACATCTCCACCTCCAGGTCGGGACGGGAGTCTTAACGCT 1902
484 ysthAlaAsnAsnSerAlaGlyValValLeuTyrGlnAlaArgIleAsn 500
1903 GCACGTGCCACACTCGGCGGAGTGTCTGTATTCAGGCTCGAATAAAC 1952
501 ValArgGlyProAlaSerIleArgProHeLysAsnIleThrAlaIleAl 517
1953 GTACAGCGGCTGCACAAKATTCGACCAATCAAAAACATCACAGCAATTC 2002
517 aGlyArgAspThrTyrIleHisCysArgValIleGlyTyrProTyrTyrS 534
2003 AGCAGCGGAGACATTAATCACTGCTGCTGTGATGCTATCCGTTACT 2052
534 eTlleLysTrpTyrLysAsnSerAsnLeuLeuProPheAsnHisArgGln 550
2053 CCATTAAATGGTAACAAGACTTAACCTGCTCTTCAACACCGCCGCA 2102
551 ValAlaPheGluAsnAsnGlyThrLeuLysLeuSerAspValGlnLysG 567
2103 GTGGCAATTTGAGAACAAATGAACCTTAACCTTAACTTAAAGTGTCAAAAAGGA 2152
567 uValAspGluGlyGluTyrThrCysAsnValLeuValGlnProGlnLeuS 584
2153 AGTGGACAGAGGAGATACACGTGCAACGTGTGGTCAACCAACAACCTCT 2202
584 eThrSerGlnSerValHisValThrValLysValProProHeIleGln 600
2203 CCACAGCCAGACGCTCCACCTGACCGTGAAGTTCCCTTTCATACAA 2252
601 ProPheGluPheProArgPheSerIleGlyGlnArgValPheIleProCy 617

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[illegible]

834	gTyrLeuValSerThrLysGluValGlyGluGluValIle.....Sert	849
1125	TTATTTT.....	1150
849	hIleuGlnIleLeuProThrValArgGluAspSerGlyPhePheSerCys	865
1151	ACTTACGGTACTCTGGGTGGTGAAGTCACATGATGAAGCTTTTATCATCT	1200
866	HisAlaIleAsnSerTyrGlyGluAspArgIleIleGlnLeuThr	882
1201	GGGGCTGAATAATGAGGCTGGAAATGCCCAGACACGTGCACAGCTCATGT	1250
882	IleGlnIu.....ProAspProProG	890
1251	CCCTACAGCTGCATCCCAAGCTCCAGTCTCTCTCCGTGGCTCCACAG	1300
890	IuIleGluIleLysAspValLysAlaArgThrIleThrLeuArgTyrPthr	906
1301	ARGTGTCCTCTGTGGTTTCACCCGATTTGGTCGCTCAGCTGGCGC	1350
907	MetGlyPheAspGlyAsnSerProIleThrGlyTyrAspIleGlyCysIy	923
1351	CCACCTGCAGAAAGCAGAAAGCAACATTCAAACTTCACGCGCTTTTCTC	1400
923	AsnLysSerAspSerTyrPaspSerAlaGlnArgThrLysAspAlSer	940
1401	CAGAGAGGTGACACACAGCAGACGACATTGATATACACACAGCTGGT	1450
940	ro...GlnLeuAsnSerAlaThrIleIleAspIleHisProSerSerThr	955
1451	CCCTTCAGCTC.....ACTGGGGAACCTGCAGACCCAGAAAGCATG	1491
956	TyrSerIleArgMetLysValLysAsnArgIleGlyLysSerGluProse	972
1492	TACACCTTTCGAGTTGTGGCTTACATATGAATGGGACGGGAGAGATT	1541
972	rAsnGluLeuThrIleThrAlaAsp...GluAlaAlaProaspGlyProp	988
1542	TCAACCATTCAGAGTGGCCACACACAGCTGAGTTCGACAGGCGCAG	1591
988	roGlnIuValHisLeuGluProIleSerSerGlnSerIleArgValThr	1004
1592	TACAAAACCTGCAGAGCTGATGTACCTCACTCACTCAATTTTATTACC	1641
1005	TrpLysAlaProLysLysHisLeuLnsnGlyIleIleArgLysTyrG	1021
1642	TGGGAGACCCCT.....GCTATGCAAAAGCTGACAGCTTATACG	1685
1021	nIleGlyTyrArgGlnTyrSerIleArgLysLysAsnGlnPheAsnIleI	1038
1686	ATTGTTCTGCACGACAGCTGCTACAGAAACAGCAATATAGAGTT	1734
1038	IleSerValAspThrSerGlyAspSerGluValTyrThrLeuAspAsnLeu	1054
1735GATGACATCTTATAACTGGAAGCGCTG	1764
1055	AsnLysPheThrGlnTyrGlyLeuValGlnAlaCysAsnArgAlaG	1071
1765	AAAAATTCACCAATATATGCTTTCATCTTACCTTATTAATCGCTATG	1814
1071	YrHngLysProSerSerGlnGluIleIleThrThrThrLeuGluAspValP	1088
1815	TCCGGGGGTCTTACAGATGATATACAGCTGGTTCACACTTCTGACGTGC	1864
1088	roSerTyrProProGluAsnValGlnAlaIleAlaThrSerProGluSer	1104
1865	CAAGTGCAGCCGCTCAGAACGTCCTCCCTGGAAGTGTATCATTCAGAGAGT	1914
1105	IleSerIleSerTyrPserThrIleuSerLysGluAlaLeuAsnGlyIleIle	1121
1915	ATTCAAATTTAGCTGGCTGCTCTCCATCAGGACACAAATAGGATTTAT	1964
1121	uGlnGlyPheArgValIleTyrTrpLysAsnLeuIleAspGlyGluLeuG	1138